

C. Kaufman

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/955,572A

DATE: 11/05/1998
TIME: 16:17:59

Input Set: H955572A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format

1 <110> APPLICANT: Kwon, Byoung
2 <120> TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
3 METHODS
4 <130> FILE REFERENCE: 740.013US2
5 <140> CURRENT APPLICATION NUMBER: US/08/955,572A
6 <141> CURRENT FILING DATE: 1998-10-22
7 <150> EARLIER APPLICATION NUMBER: 08/461,652
8 <151> EARLIER FILING DATE: 1995-06-05
9 <150> EARLIER APPLICATION NUMBER: 08/122,796
10 <151> EARLIER FILING DATE: 1993-09-03
11 <160> NUMBER OF SEQ ID NOS: 10
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 838
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
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19 catagtagcc actctgttgc tggctctcaa ctttgagagg acaagatcat tgcaggatcc 120
20 ttgtagtaac tgcccagctg gtacattctg tgataataac aggaatcaga tttgcagtc 180
21 ctgtcctcca aatagtttct ccagcgagcagg tggacaaagg acctgtgaca tatgcaggca 240
22 gtgtaaagggt gttttcagga ccaggaagga gtgttcctcc accagcaatg cagagtgtga 300
23 ctgcactcca gggtttctact gacctggggc aggatgcagc atgtgtgaac aggattgtaa 360
24 acaaggtcaa gaactgacaa aaaaagggtg taaagactgt tgctttggga catttaacga 420
25 tcagaaacgt ggcatctgtc gacctggac aaactgttct ttggatggaa agtctgtgct 480
26 tgtgaatggg acgaaggaga gggacgtggg ctgtggacca tctccagctg acctctctcc 540
27 gggagcatcc tctgtgacct cgctgcccc tgcgagagag ccaggacact ctccgcagat 600
28 catctccttc tttcttgccg tgacgtcgac tgcgttgctc ttctgtgtgt tcttctctac 660
29 gctccgtttc tctgttggtt aacggggcag aaagaaactc ctgtatatat tcaaacaacc 720
30 atttatgaga ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga 780
31 agaagaagaa ggaggatgtg aactgtgaaa tggaagtcaa tagggctgtt gggacttt 838

Does Not Comply
Corrected Diskette Needed

32 <210> SEQ ID NO 2
33 <211> LENGTH: 255
34 <212> TYPE: PRT
35 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 2
37 Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
38 1 5 10 15
39 Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
40 20 25 30
41 Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
42 35 40 45
43 Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
44 50 55 60

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45      Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
46      65                      70                      75                      80
47      Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
48                      85                      90                      95
49      Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
50                      100                     105                     110
51      Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
52                      115                     120                     125
53      Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
54                      130                     135                     140
55      Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
56      145                      150                      155                      160
57      Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
58                      165                      170                      175
59      Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
60                      180                      185                      190
61      Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
62                      195                      200                      205
63      Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
64                      210                      215                      220
65      Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
66      225                      230                      235                      240
67      Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
68                      245                      250                      255

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69 <210> SEQ ID NO 3

70 <211> LENGTH: 20

71 <212> TYPE: DNA

72 <213> ORGANISM: Homo sapiens

73 <400> SEQUENCE: 3

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76 <211> LENGTH: 20

77 <212> TYPE: DNA

78 <213> ORGANISM: Homo sapiens

79 <400> SEQUENCE: 4

80 ttytcstsca htggtggaca

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81 <210> SEQ ID NO 5

82 <211> LENGTH: 20

83 <212> TYPE: DNA

84 <213> ORGANISM: Homo sapiens

85 <400> SEQUENCE: 5

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20

87 <210> SEQ ID NO 6

88 <211> LENGTH: 20

89 <212> TYPE: DNA

90 <213> ORGANISM: Homo sapiens

91 <400> SEQUENCE: 6

92 ttytgtrcrt traatgttcc

20

93 <210> SEQ ID NO 7

94 <211> LENGTH: 25

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RAW SEQUENCE LISTING
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96 <213> ORGANISM: Homo sapiens
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100 <211> LENGTH: 30
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
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106 <211> LENGTH: 2350
107 <212> TYPE: DNA
108 <213> ORGANISM: Mus musculus
109 <400> SEQUENCE: 9
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112 tgtcctgtgc atgtgacatt tcgccatggg aaacaactgt tacaacgtgg tggtcattgt 180
113 gctgctgcta gtgggctgtg agaaggtggg agcctgtcag aactcctgtg ataactgtca 240
114 gcctggtaact ttctgcagaa aatacaatcc agtctgcaag agctgccctc caagtacctt 300
115 ctccagcata ggtggacagc cgaactgtaa catctgcaga gtgtgtgcag gctatttcag 360
116 gttcaagaag ttttgctcct ctaccacaa cgcgagtggt gagtgcattg aaggattcca 420
117 ttgcttgggg ccacagtga ccagatgtga aaaggactgc aggcctggcc aggagctaac 480
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123 atggatcagg aaaaaattcc ccacatatatt caagcaacca ttaagaaga cactggagc 840
124 agctcaagag gaagatgctt gtagctgccg atgtccacag gaagaagaag gaggaggagg 900
125 aggctatgag ctgtgatgta ctatcctagg agatgtgtgg gccgaaaccg agaagcacta 960
126 ggacccacc atcctgtgga acagcacaag caacccacc accctgttct tacacatcat 1020
127 cctagatgat gtgtgggcgc gcacctcatc caagtctctt ctaacgctaa catatttgtc 1080
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129 ctgtatgcac acgtgtgtgt gtgtgtgtgt gtgacactcc tgatgctga ggaggtcaga 1200
130 *all* *item* *10 m* *Enu* *hmm* *hst* agacaaaggg ttggttccat aagaactgga gttatggatg gctgtgagcc ggnngatag 1260
131 gtcgggacgg agacctgtct tcttatttta acgtgactgt ataataaaaa aaaaatgata 1320
132 tttcgggaat tgtagagatt gtcctgacac ctttctagtt aatgatctaa gaggaattgt 1380
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143 tggcgccaag ataaaaaac caaaagcctt gactccggtg ctaattctcc ctgccggccc 2040
144 ccgtaagcat aacgcggcga tctccacttt aagaacctgg ccgcgttctg cctgggtctcg 2100

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145      ctttcgtaaa cggttccttac aaaagtaatt agttcttgct ttcagcctcc aagcttctgc      2160
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147      agggtaactgg gcggcccgtc gaaggccctt tggtttcaga aacccaaggc cccctcata      2280
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151 <211> LENGTH: 256
152 <212> TYPE: PRT
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154 <400> SEQUENCE: 10
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158      20              25              30
159      Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
160      35              40              45
161      Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
162      50              55              60
163      Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
164      65              70              75              80
165      His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
166      85              90              95
167      Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
168      100             105             110
169      Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
170      115             120             125
171      Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
172      130             135             140
173      Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
174      145             150             155             160
175      Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
176      165             170             175
177      Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
178      180             185             190
179      Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
180      195             200             205
181      Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
182      210             215             220
183      Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
184      225             230             235             240
185      Cys Arg Cys Pro Gln Glu Glu Gly Gly Gly Gly Tyr Glu Leu
186      245             250             255

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VERIFICATION SUMMARY
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DATE: 11/05/1998
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Line	? Error/Warning	Original Text
130	W "N" or "Xaa" used: Feature required	agacaaaggg ttggttccat aagaactgga gttatgga

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: _____

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminoes The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 _____ Wrong Designation Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence Id number
<400> sequence Id number
000
- 10 _____ Use of N's or Xaa's (NEW RULES) Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 _____ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 _____ Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98

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